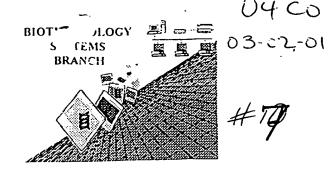# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/778,187_

Source: _OIPE_

Date Processed by STIC: _3-1-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable-form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING   DATE: 03/01/2001
PATENT APPLICATION: US/09/778,187   TIME: 14:59:56

Does Not Comply
Corrected Diskette Needed
See pp. 1, 3

Input Set : A:\2873-US seq.txt
Output Set: N:\CRF3\03012001\I778187.raw

```
      4 <110> APPLICANT: Baum, Peter Robert
      5          Fanslow III, William C.
      7 <120> TITLE OF INVENTION: Molecules Designated LDCAM
      9 <130> FILE REFERENCE: 2873-US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/778,187  <───
     12 <141> CURRENT FILING DATE: 2001-02-06
W--> 14 <140> CURRENT APPLICATION NUMBER: PCT/US99/17905 ───>
     15 <141> CURRENT FILING DATE: 1999-08-05
     17 <150> PRIOR APPLICATION NUMBER: 60/095,672
     18 <151> PRIOR FILING DATE: 1998-08-07
     20 <160> NUMBER OF SEQ ID NOS: 10
     22 <170> SOFTWARE: PatentIn Ver. 2.0
```

There can be only one current application number and date. All others should be under <150>, <151>

ERRORED SEQUENCES

```
     25 <210> SEQ ID NO: 1
     26 <211> LENGTH: 1535  ───>
     27 <212> TYPE: DNA
     28 <213> ORGANISM: Homo sapien
     30 <220> FEATURE:
     31 <221> NAME/KEY: CDS
     32 <222> LOCATION: 16..1341
     34 <400> SEQUENCE: 1
     36 gcggccgcgc ccgac atg gcg agt gta gtg ctg ccg agc gga tcc cag tgt    51
     37                   Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys
     38                    1               5                  10
     40 gcg gcg gca gcg gcg gcg gcg gcg cct ccc ggg ctc cgg ctc cgg ctt    99
     41 Ala Ala Ala Ala Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu
     42          15                  20                  25
     44 ctg ctg ttg ctc ttc tcc gcc gcg gca ctg atc ccc aca ggt gat ggg   147
     45 Leu Leu Leu Leu Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly
     46      30                  35                  40
     48 cag aat ctg ttt acg aaa gac gtg aca gtg atc gag gga gag gtt gcg   195
     49 Gln Asn Leu Phe Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala
     50  45                  50                  55                  60
     52 acc atc agt tgc caa gtc aat aag agt gac gac tct gtg att cag cta   243
     53 Thr Ile Ser Cys Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu
     54              65                  70                  75
     56 ctg aat ccc aac agg cag acc att tat ttc agg gac ttc agg cct ttg   291
     57 Leu Asn Pro Asn Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu
     58              80                  85                  90
     60 aag gac agc agg ttt cag ttg ctg aat ttt tct agc agt gaa ctc aaa   339
     61 Lys Asp Ser Arg Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys
     62          95                 100                 105
     64 gta tca ttg aca aac gtc tca att tct gat gaa gga aga tac ttt tgc   387
     65 Val Ser Leu Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys
```

Number of bases differ:
-1535 listed
-1598 shown

RAW SEQUENCE LISTING   DATE: 03/01/2001
PATENT APPLICATION: US/09/778,187   TIME: 14:59:56

Input Set : A:\2873-US seq.txt
Output Set: N:\CRF3\03012001\I778187.raw

```
66      110                115                120
68 cag ctc tat acc gat ccc cca cag gaa agt tac acc acc atc aca gtc   435
69 Gln Leu Tyr Thr Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val
70 125               130                135                140
72 ctg gtc cca cca cgt aat ctg atg atc gat atc cag aaa gac act gcg   483
73 Leu Val Pro Pro Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala
74                145                150                155
76 gtg gaa ggt gag gag att gaa gtc aac tgc act gct atg gcc agc aag   531
77 Val Glu Gly Glu Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys
78                160                165                170
80 cca gcc acg act atc agg tgg ttc aaa ggg aac aca gag cta aaa ggc   579
81 Pro Ala Thr Thr Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly
82           175                180                185
84 aaa tcg gag gtg gaa gag tgg tca gac atg tac act gtg acc agt cag   627
85 Lys Ser Glu Val Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln
86      190                195                200
88 ctg atg ctg aag gtg cac aag gag gac gat ggg gtc cca gtg atc tgc   675
89 Leu Met Leu Lys Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys
90 205               210                215                220
92 cag gtg gag cac cct gcg gtc act gga aac ctg cag acc cag cgg tat   723
93 Gln Val Glu His Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr
94                225                230                235
96 cta gaa gta cag tat aag cct caa gtg cac att cag atg act tat cct   771
97 Leu Glu Val Gln Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro
98           240                245                250
100 cta caa ggc tta acc cgg gaa ggg gac gcg ctt gag tta aca tgt gaa   819
101 Leu Gln Gly Leu Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu
102          255                260                265
104 gcc atc ggg aag ccc cag cct gtg atg gta act tgg gtg aga gtc gat   867
105 Ala Ile Gly Lys Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp
106      270                275                280
108 gat gaa atg cct caa cac gcc gta ctg tct ggg ccc aac ctg ttc atc   915
109 Asp Glu Met Pro Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile
110 285               290                295                300
112 aat aac cta aac aaa aca gat aat ggt aca tac cgc tgt gaa gct tca   963
113 Asn Asn Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser
114                305                310                315
116 aac ata gtg ggg aaa gct cac tcg gat tat atg ctg tat gta tac gat   1011
117 Asn Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp
118           320                325                330
120 ccc ccc aca act atc cct cct ccc aca aca acc acc acc acc acc acc   1059
121 Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr
122          335                340                345
124 acc acc acc acc acc atc ctt acc atc atc aca gat tcc cga gca ggt   1107
125 Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly
126      350                355                360
128 gaa gaa ggc tcg atc agg gca gtg gat cat gcc gtg atc ggt ggc gtc   1155
129 Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val
130 365               370                375                380
```

```
    132 gtg gcg gtg gtg gtg ttc gcc atg ctg tgc ttg ctc atc att ctg ggg  1203
    133 Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly
    134             385             390             395
    136 cgc tat ttt gcc aga cat aaa ggt aca tac ttc act cat gaa gcc aaa  1251
    137 Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys
    138             400             405             410
    140 gga gcc gat gac gca gca gac gca gac aca gct ata atc aat gca gaa  1299
    141 Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
    142         415             420             425
    144 gga gga cag aac aac tcc gaa gaa aag aaa gag tac ttc atc          1341
    145 Gly Gly Gln Asn Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile
    146     430             435             440
    148 tagatcagcc tttttgtttc aatgaggtgt ccaactggcc ctatttagat gataaagaga  1401
    150 cagtgatatt ggaacttgcg agaaattcgt gtgttttttt atgaatgggt ggaaaggtgt  1461
    152 gagactggga aggcttggga tttgctgtgt aaaaaaaaaa aaaaaatgtt ctttggaaag  1521
    154 aaaaaagcgg ccgctttctt attctatttc aacattcagc ttaatcataa tcctaaaatc  1581
E-->156 atacatgcta tttccat                                                 1598
    484 <210> SEQ ID NO: 5
    485 <211> LENGTH: 29
E-->486 <212> TYPE: Oligonucleotide
    487 <213> ORGANISM: Homo sapien
    489 <400> SEQUENCE: 5
    491 tatgtcgaca tggcgagtgt agtgctgcc          29
    494 <210> SEQ ID NO: 6
    495 <211> LENGTH: 30
E-->496 <212> TYPE: Oligonucleotide
    497 <213> ORGANISM: Homo sapien
    499 <400> SEQUENCE: 6
    501 atatagatct atgatccact gccctgatcg          30
```

Non-valid response for <212>

Valid responses are:

— DNA

— RNA

— PRT (Protein)

VERIFICATION SUMMARY   DATE: 03/01/2001
PATENT APPLICATION: US/09/778,187   TIME: 14:59:58

Input Set : A:\2873-US seq.txt
Output Set: N:\CRF3\03012001\I778187.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:280 W: Numeric Identifier already exists, <140> found multiple times
L:14 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:156 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1535 Found:1598 SEQ:1
L:486 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:496 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: